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<130> 1488.0360000

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<150> 60/259,853

<151> 2001-01-05

<150> 60/286,368

<151> 2001-04-26

<150> 60/331,168

<151> 2001-11-09

<160> 176

<170> PatentIn Ver. 2.1

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<211> 627

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<213> Homo sapiens

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<221> CDS

 $\langle 222 \rangle \quad (1) \dots (624)$

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ccc ggc tgc tgc tgc tgc tgc ttt ttg ttg ctg ttc ttg gtg tct tcc 96
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
20 25 30

gtc cct gtc acc tgc caa gcc ctt ggt cag gac atg gtg tca cca gag 144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
35 40 45

gcc acc aac tct tct tcc tcc tcc ttc tcc tct cct tcc agc gcg gga 192
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly

Variable	Mean	SD	Min	Max
Age	34.2	10.5	18	65
Gender	50.0	0.0	0	1
Marital status	50.0	0.0	0	1
Education	12.5	1.5	9	16
Income	12.5	1.5	9	16
Occupation	12.5	1.5	9	16
Health status	12.5	1.5	9	16
Life satisfaction	12.5	1.5	9	16
Life expectancy	12.5	1.5	9	16
Life expectancy squared	12.5	1.5	9	16
Life expectancy cubed	12.5	1.5	9	16
Life expectancy to the fourth power	12.5	1.5	9	16
Life expectancy to the fifth power	12.5	1.5	9	16
Life expectancy to the sixth power	12.5	1.5	9	16
Life expectancy to the seventh power	12.5	1.5	9	16
Life expectancy to the eighth power	12.5	1.5	9	16
Life expectancy to the ninth power	12.5	1.5	9	16
Life expectancy to the tenth power	12.5	1.5	9	16
Life expectancy to the eleventh power	12.5	1.5	9	16
Life expectancy to the twelfth power	12.5	1.5	9	16
Life expectancy to the thirteenth power	12.5	1.5	9	16
Life expectancy to the fourteenth power	12.5	1.5	9	16
Life expectancy to the fifteenth power	12.5	1.5	9	16
Life expectancy to the sixteenth power	12.5	1.5	9	16
Life expectancy to the seventeenth power	12.5	1.5	9	16
Life expectancy to the eighteenth power	12.5	1.5	9	16
Life expectancy to the nineteenth power	12.5	1.5	9	16
Life expectancy to the twentieth power	12.5	1.5	9	16
Life expectancy to the twenty-first power	12.5	1.5	9	16
Life expectancy to the twenty-second power	12.5	1.5	9	16
Life expectancy to the twenty-third power	12.5	1.5	9	16
Life expectancy to the twenty-fourth power	12.5	1.5	9	16
Life expectancy to the twenty-fifth power	12.5	1.5	9	16
Life expectancy to the twenty-sixth power	12.5	1.5	9	16
Life expectancy to the twenty-seventh power	12.5	1.5	9	16
Life expectancy to the twenty-eighth power	12.5	1.5	9	16
Life expectancy to the twenty-ninth power	12.5	1.5	9	16
Life expectancy to the thirtieth power	12.5	1.5	9	16
Life expectancy to the thirty-first power	12.5	1.5	9	16
Life expectancy to the thirty-second power	12.5	1.5	9	16
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Life expectancy to the thirty-eighth power	12.5	1.5	9	16
Life expectancy to the thirty-ninth power	12.5	1.5	9	16
Life expectancy to the fortieth power	12.5	1.5	9	16
Life expectancy to the forty-first power	12.5	1.5	9	16
Life expectancy to the forty-second power	12.5	1.5	9	16
Life expectancy to the forty-third power	12.5	1.5	9	16
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Life expectancy to the forty-sixth power	12.5	1.5	9	16
Life expectancy to the forty-seventh power	12.5	1.5	9	16
Life expectancy to the forty-eighth power	12.5	1.5	9	16
Life expectancy to the forty-ninth power	12.5	1.5	9	16
Life expectancy to the fiftieth power	12.5	1.5	9	16
Life expectancy to the fifty-first power	12.5	1.5	9	16
Life expectancy to the fifty-second power	12.5	1.5	9	16
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Life expectancy to the fifty-fifth power	12.5	1.5	9	16
Life expectancy to the fifty-sixth power	12.5	1.5	9	16
Life expectancy to the fifty-seventh power	12.5	1.5	9	16
Life expectancy to the fifty-eighth power	12.5	1.5	9	16
Life expectancy to the fifty-ninth power	12.5	1.5	9	16
Life expectancy to the sixtieth power	12.5	1.5	9	16
Life expectancy to the sixty-first power	12.5	1.5	9	16
Life expectancy to the sixty-second power	12.5	1.5	9	16
Life expectancy to the sixty-third power	12.5	1.5	9	16
Life expectancy to the sixty-fourth power	12.5	1.5	9	16
Life expectancy to the sixty-fifth power	12.5	1.5	9	16
Life expectancy to the sixty-sixth power	12.5	1.5	9	16
Life expectancy to the sixty-seventh power	12.5	1.5	9	16
Life expectancy to the sixty-eighth power				

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Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly			
	85	90	95
aag gtc agc ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag			336
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu			
	100	105	110
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Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser			
	115	120	125
aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa			432
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys			
	130	135	140
gaa ttt aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga			480
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly			
	145	150	155
tac aat acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg			528
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met			
	165	170	175
tat gtg gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca			576
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr			
	180	185	190
cga agg aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca			624
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Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu			
	35	40	45
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly			
	50	55	60
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg			
	65	70	75
			80

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Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
85 90 95

Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
100 105 110

Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
115 120 125

Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
130 135 140

Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
145 150 155 160

Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
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Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
180 185 190

Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
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Thr Ala Pro Asn Gly Thr Leu Glu Ala Glu Leu Glu Arg Arg Trp Glu
35 40 45
Ser Leu Val Ala Leu Ser Leu Ala Arg Leu Pro Val Ala Ala Gln Pro
50 55 60
Lys Glu Ala Ala Val Gln Ser Gly Ala Gly Asp Tyr Leu Leu Gly Ile
65 70 75 80
Lys Arg Leu Arg Arg Leu Tyr Cys Asn Val Gly Ile Gly Phe His Leu
85 90 95
Gln Ala Leu Pro Asp Gly Arg Ile Gly Gly Ala His Ala Asp Thr Arg
100 105 110
Asp Ser Leu Leu Glu Leu Ser Pro Val Glu Arg Gly Val Val Ser Ile
115 120 125

2040T0"010400T

Phe Gly Val Ala Ser Arg Phe Phe Val Ala Met Ser Ser Lys Gly Lys
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 Leu Tyr Gly Ser Pro Phe Phe Thr Asp Glu Cys Thr Phe Lys Glu Ile
 145 150 155 160
 Leu Leu Pro Asn Asn Tyr Asn Ala Tyr Glu Ser Tyr Lys Tyr Pro Gly
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 180 185 190
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 195 200 205

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 35 40 45
 Ser Arg Ser Arg Ala Gly Leu Ala Gly Glu Ile Ala Gly Val Asn Trp
 50 55 60
 Glu Ser Gly Tyr Leu Val Gly Ile Lys Arg Gln Arg Arg Leu Tyr Cys
 65 70 75 80
 Asn Val Gly Ile Gly Phe His Leu Gln Val Leu Pro Asp Gly Arg Ile
 85 90 95
 Ser Gly Thr His Glu Glu Asn Pro Tyr Ser Leu Leu Glu Ile Ser Thr
 100 105 110
 Val Glu Arg Gly Val Val Ser Leu Phe Gly Val Arg Ser Ala Leu Phe
 115 120 125
 Val Ala Met Asn Ser Lys Gly Arg Leu Tyr Ala Thr Pro Ser Phe Gln
 130 135 140
 Glu Glu Cys Lys Phe Arg Glu Thr Leu Leu Pro Asn Asn Tyr Asn Ala
 145 150 155 160
 Tyr Glu Ser Asp Leu Tyr Gln Gly Thr Tyr Ile Ala Leu Ser Lys Tyr
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 180 185 190
 His Phe Leu Pro Arg Ile
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 Gly Pro Ala Ala Thr Asp Arg Asn Pro Arg Gly Ser Ser Ser Arg Gln
 35 40 45
 Ser Ser Ser Ser Ala Met Ser Ser Ser Ser Ala Ser Ser Ser Pro Ala
 50 55 60
 Ala Ser Leu Gly Ser Gln Gly Ser Gly Leu Glu Gln Ser Ser Phe Gln
 65 70 75 80
 Trp Ser Pro Ser Gly Arg Arg Thr Gly Ser Leu Tyr Cys Arg Val Gly
 85 90 95
 Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys Val Asn Gly Ser
 100 105 110
 His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe Ala Val Ser Gln
 115 120 125
 Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys Phe Leu Ala Met
 130 135 140
 Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe Thr Asp Asp Cys
 145 150 155 160
 Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn Thr Tyr Ala Ser
 165 170 175
 Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp Tyr Val Ala Leu
 180 185 190
 Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro Arg Val Lys Pro
 195 200 205
 Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys Gln Ser Glu Gln
 210 215 220
 Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys Lys Asn Pro Pro
 225 230 235 240
 Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro Arg Lys Asn Thr
 245 250 255
 Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly
 260 265

<210> 16
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Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
 1 5 10 15
 Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
 20 25 30
 Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
 35 40 45
 Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
 50 55 60
 Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu
 65 70 75 80
 Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
 85 90 95
 Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr
 100 105 110
 Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
 115 120 125
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 130 135 140
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 20 25 30
 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
 35 40 45
 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
 50 55 60
 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
 65 70 75 80
 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
 85 90 95
 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
 100 105 110
 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
 115 120 125

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Met His Lys Trp Ile Leu Thr Trp Ile Leu Pro Thr Leu Leu Tyr Arg
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Ser Cys Phe His Ile Ile Cys Leu Val Gly Thr Ile Ser Leu Ala Cys
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Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser Ser
35 40 45
Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile
50 55 60
Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp
65 70 75 80
Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn
85 90 95
Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly
100 105 110
Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr
115 120 125
Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu
130 135 140
Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly
145 150 155 160
Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val Arg Gly
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Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala
180 185 190
Ile Thr

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35 40 45
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
50 55 60
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
65 70 75 80
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly

	85		90		95
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	100		105		110
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	115		120		125
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys	130		135		140
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly	145		150		155
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met	165		170		175
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Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	195		200		205

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 35 40 45
 Tyr Cys Ala Thr Lys Tyr His Leu Gln Leu His Pro Ser Gly Arg Val
 50 55 60
 Asn Gly Ser Leu Glu Asn Ser Ala Tyr Ser Ile Leu Glu Ile Thr Ala
 65 70 75 80
 Val Glu Val Gly Ile Val Ala Ile Arg Gly Leu Phe Ser Gly Arg Tyr
 85 90 95
 Leu Ala Met Asn Lys Arg Gly Arg Leu Tyr Ala Ser Glu His Tyr Ser
 100 105 110
 Ala Glu Cys Glu Phe Val Glu Arg Ile His Glu Leu Gly Tyr Asn Thr
 115 120 125
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Pro	Gly	Ala	Gly	Asn	Pro	Ala	Asp	Thr	Leu	Gly	Gln	Gly	His	Glu	Asp	
		35					40					45				
Arg	Pro	Phe	Gly	Gln	Arg	Ser	Arg	Ala	Gly	Lys	Asn	Phe	Thr	Asn	Pro	
	50					55					60					
Ala	Pro	Asn	Tyr	Pro	Glu	Glu	Gly	Ser	Lys	Glu	Gln	Arg	Asp	Ser	Val	
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Leu	Pro	Lys	Val	Thr	Gln	Arg	His	Val	Arg	Glu	Gln	Ser	Leu	Val	Thr	
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Asp	Gln	Leu	Ser	Arg	Arg	Leu	Ile	Arg	Thr	Tyr	Gln	Leu	Tyr	Ser	Arg	
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Met	Ala	Glu	Asp	Gly	Asp	Pro	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp	
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Thr	Phe	Gly	Ser	Arg	Val	Arg	Val	Arg	Gly	Ala	Glu	Thr	Gly	Leu	Tyr	
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Ile	Cys	Met	Asn	Lys	Lys	Gly	Lys	Leu	Ile	Ala	Lys	Ser	Asn	Gly	Lys	
				165					170					175		
Gly	Lys	Asp	Cys	Val	Phe	Thr	Glu	Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr	
			180					185					190			
Ala	Leu	Gln	Asn	Ala	Lys	Tyr	Glu	Gly	Trp	Tyr	Met	Ala	Phe	Thr	Arg	
		195					200					205				
Lys	Gly	Arg	Pro	Arg	Lys	Gly	Ser	Lys	Thr	Arg	Gln	His	Gln	Arg	Glu	

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Val His Phe Met Lys Arg Leu Pro Arg Gly His His Thr Thr Glu Gln		
225	230	235 240
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Arg Gly Ser Gln Arg Thr Trp Ala Pro Glu Pro Arg		
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 ccaacaccac caacgccacc accagctcct gctgctgcgg ccacccacgt ccaccattta 360
 ccgggaggct ccagaggcgt aggcagcgg tccgagaaag gagcgagggg agtcagccgg 420
 cttttccgag gagttatgga tggttggtgca ttcacttctg gccagatccg cgccagagg 480
 gagctaacca gcagccacca cctcgagctc tctccttgcc ttgcatcggg tttaccctt 540
 ccagtatgtt ctttctgatg agacaatttc cagtgccgag agtttcagta ca atg tgg 598
 Met Trp
 1

aaa tgg ata ctg aca cat tgt gcc tca gcc ttt ccc cac ctg ccc ggc	646
Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro Gly	
5 10 15	

tgc tgc tgc tgc tgc ttt ttg ttg ctg ttc ttg gtg tct tcc gtc cct	694
Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val Pro	
20 25 30	

gtc acc tgc caa gcc ctt ggt cag gac atg gtg tca cca gag gcc acc	742
Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
35 40 45 50	

aac tct tct tcc tcc tcc ttc tcc tct cct tcc agc gcg gga agg cat	790
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
55 60 65	

gtg cgg agc tac aat cac ctt caa gga gat gtc cgc tgg aga aag cta	838
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	

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70	75	80	
ttc tct ttc acc aag tac ttt ctc aag att gag aag aac ggg aag gtc			886
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val			
85	90	95	
agc ggg acc aag aag gag aac tgc cgc tac agc atc ctg gag ata aca			934
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr			
100	105	110	
tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat			982
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr			
115	120	125	130
tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt			1030
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe			
	135	140	145
aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga tac aat			1078
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn			
	150	155	160
acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg tat gtg			1126
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val			
	165	170	175
gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca cga agg			1174
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg			
	180	185	190
aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca			1216
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser			
	195	200	205
tagaggaagg caacgtttgt ggatgcagta aaaccaatgg ctcttttgcc aagaatagtg			1276
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ttaaaagaaa gccagccttt gaaggttttt gtattcactg ctgacatatg atgttctttt			1396
aattagttct gtgtcatgtc ttataatcaa gatataggca gatcgaatgg gatagaagtt			1456
attcccaagt gaaaaacatt gtggctgggt tttttgttgt tgttgtcaag tttttgtttt			1516
taaacctctg agatagaact taaaggacat agaacaatct gttgaaagaa cgatcttcgg			1576
gaaagttatt tatggaatac gaactcatat caaagacttc attgctcatt caagccta			1636
gaatcaatga acagtaatac gtgcaagcat ttactggaaa gcacttgggt catatcatat			1696
gcacaaccaa aggagttctg gatgtggtct catggaataa ttgaatagaa tttaaaaata			1756
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tgccttcac cctttctatt tctttctaag ttatttattt aataggatgt taaatatctt			1876
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cacaccacat gcatgttcac gacaaagtgt ttttaaaact tggcgaacac ttcaaaaata			1996
ggagttggga ttagggaagc agtatgagtg cccgtgtgct atcagttgac ttaatttgca			2056

cttctgcagt aataaccatc aacaataaat atggcaatgc tgtgccatgg cttgagtga 2116
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aaagaaagag agaaaagaca gaaagacagg aaggaaggaa ggaaggaagg aaggaaggaa 3916

ggaagcaagg aaagaaggaa ggaaggaaaag aagggaggga aggaaggaga gagaaagaaa 3976
gattgtttgg taaggagtaa tgacattctc ttgcatttaa aagtggcata tttgcttgaa 4036
atggaaatag aattctgggc ccttttgcaa ctactgaaga aaaaaaaaag cagtttcagc 4096
cctgaatgtt gtagatttga aaaaaaaaaa aaaaaaactc gaggggggggc ccgtacccaa 4156
ttcgccctat agtgagtcgt a 4177

<210> 24
<211> 208
<212> PRT
<213> Homo sapiens

<400> 24
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
1 5 10 15
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
20 25 30
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
35 40 45
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
50 55 60
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
65 70 75 80
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
85 90 95
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
100 105 110
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
115 120 125
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
130 135 140
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
145 150 155 160
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
165 170 175
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
180 185 190
Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
195 200 205

<210> 25
<211> 31
<212> PRT
<213> Homo sapiens

1003642040

<400> 25

Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser
1 5 10 15

Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn
20 25 30

<210> 26

<211> 19

<212> PRT

<213> Homo sapiens

<400> 26

Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys
1 5 10 15

Pro Tyr Ser

<210> 27

<211> 30

<212> PRT

<213> Homo sapiens

<400> 27

Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys
1 5 10 15

Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr
20 25 30

<210> 28

<211> 19

<212> PRT

<213> Homo sapiens

<400> 28

Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn
1 5 10 15

Thr Ser Ala

<210> 29

<211> 555

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(552)

<220>

<223> Description of Artificial Sequence: pQE60-Cys37
construct

<400> 29

atg aga gga tcg cat cac cat cac cat cac gga tcc tgc cag gct ctg 48

Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Ser	Cys	Gln	Ala	Leu	
1				5					10					15		
ggt	cag	gac	atg	gtt	tct	cag	gaa	gct	acc	aac	tct	tcc	tct	tcc	tct	96
Gly	Gln	Asp	Met	Val	Ser	Pro	Glu	Ala	Thr	Asn	Ser	Ser	Ser	Ser	Ser	
			20					25					30			
ttc	tct	tcc	ccg	tct	tcc	gct	ggg	cgt	cac	gtt	cgt	tct	tac	aac	cac	144
Phe	Ser	Ser	Pro	Ser	Ser	Ala	Gly	Arg	His	Val	Arg	Ser	Tyr	Asn	His	
		35					40				45					
ctg	cag	ggg	gac	gtt	cgt	tgg	cgt	aaa	ctg	ttc	tct	ttc	acc	aaa	tac	192
Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	
	50					55					60					
ttc	ctg	aaa	atc	gaa	aaa	aac	ggg	aaa	gtt	tct	ggg	acc	aag	aag	gag	240
Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	
65					70				75						80	
aac	tgc	ccg	tac	agc	atc	ctg	gag	ata	aca	tca	gta	gaa	atc	gga	gtt	288
Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	
				85					90					95		
gtt	gcc	gtc	aaa	gcc	att	aac	agc	aac	tat	tac	tta	gcc	atg	aac	aag	336
Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	
			100					105					110			
aag	ggg	aaa	ctc	tat	ggc	tca	aaa	gaa	ttt	aac	aat	gac	tgt	aag	ctg	384
Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	
		115					120					125				
aag	gag	agg	ata	gag	gaa	aat	gga	tac	aat	acc	tat	gca	tca	ttt	aac	432
Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	
	130					135					140					
tgg	cag	cat	aat	ggg	agg	caa	atg	tat	gtg	gca	ttg	aat	gga	aaa	gga	480
Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	
145				150					155					160		
gct	cca	agg	aga	gga	cag	aaa	aca	cga	agg	aaa	aac	acc	tct	gct	cac	528
Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	
				165				170						175		
ttt	ott	cca	atg	gtg	gta	cac	tca	tag								555
Phe	Leu	Pro	Met	Val	Val	His	Ser									
			180													

<210> 30

<211> 184

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pQE60-Cys37 construct

<400> 30

Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Ser	Cys	Gln	Ala	Leu	
1				5					10					15		

Gly	Gln	Asp	Met	Val	Ser	Pro	Glu	Ala	Thr	Asn	Ser	Ser	Ser	Ser	Ser	
			20					25					30			

Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His
35 40 45

Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr
50 55 60

Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu
65 70 75 80

Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val
85 90 95

Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys
100 105 110

Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
115 120 125

Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn
130 135 140

Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly
145 150 155 160

Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
165 170 175

Phe Leu Pro Met Val Val His Ser
180

<210> 31
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 31
atgtggaaat ggatactgac ccactgcgct tctgctttcc cgcacctgcc gggttgctgc 60
tgctgctgct tctgctgct gtcc 84

<210> 32
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 32
ccggagaaac catgtcctga cccagagcct ggcaggtaac cggaacagaa gaaaccagga 60
acagcagcag gaagcagcag ca 82

<210> 33
<211> 80

<220>
<223> Description of Artificial Sequence: synthetic primer

<400> 37
aaagatcca tgtggaaatg gatactgacc cactgc 36

<210> 38
<211> 627
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(627)

<400> 38
atg tgg aaa tgg ata ctg acc cac tgc gct tct gct ttc ccg cac ctg 48
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
1 5 10 15

ccg ggt tgc tgc tgc tgc tgc ttc ctg ctg ctg ttc ctg gtt tct tct 96
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
20 25 30

gtt ccg gtt acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa 144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
35 40 45

gct acc aac tct tcc tct tcc tct ttc tct tcc ccg act tcc gct ggt 192
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Thr Ser Ala Gly
50 55 60

cgt cac gtt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt 240
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
65 70 75 80

aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa atc gaa aaa aac ggt 288
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
85 90 95

aaa gtt tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag 336
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu
100 105 110

ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc 384
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser
115 120 125

aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa 432
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys
130 135 140

gaa ttt aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga 480
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly
145 150 155 160

tac aat acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg 528
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
165 170 175

tat gtg gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca 576
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
180 185 190

624

627

<210> 39

<211> 208

<212> PRT

<213> Escherichia coli

<400> 39

Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
1 5 10 15

Pro Gly Cys Cys Cys Cys Phe Leu Leu Phe Leu Val Ser Ser

Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu

Ala Thr Asn Ser Ser Ser Ser Phe Ser Ser Pro Thr Ser Ala Gly

Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg

Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly

Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu

Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser

Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys

Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly

145 Tyr Asn Thr Tyr Ala 150 Ser Phe Asn Trp Gln 155 His Asn Gly Arg Gln 160 Met
165 170 175

Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr

Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser

<210> 40

<211> 38

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: primer

<400> 40

tttcatgact tgtcaagctc tgggtcaaga tatgggtc

<210> 41

<211> 28

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: primer

<400> 41
gccaagctt ccacaaacgt tgccttcc

28

<210> 42
<211> 525
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(522)

<400> 42
atg acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa gct acc 48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15
aac tct tcc tct tcc tct ttc tct tcc ccg tct tcc gct ggt cgt cac 96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30
gtt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt aaa ctg 144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45
ttc tct ttc acc aaa tac ttc ctg aaa atc gaa aaa aac ggt aaa gtt 192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60
tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca 240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80
tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat 288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95
tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt 336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110
aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga tac aat 384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125
acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg tat gtg 432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140
gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca cga agg 480
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160
aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca tag 525
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

<210> 43
<211> 174
<212> PRT

20250304

<213> Escherichia coli

<400> 43

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Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
 1              5              10              15

Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
      20              25              30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
      35              40              45

Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
      50              55              60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
      65              70              75              80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
      85              90              95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
      100              105              110

Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
      115              120              125

Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
      130              135              140

Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
      145              150              155              160

Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
      165              170
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<210> 44

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic primer

<400> 44

tcagtgaatt cattaagag gagaaattaa tcatgacttg ccagg

45

<210> 45

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic primer

<400> 45

tcatgacttg ccaggcactg ggtcaagaca tggtttcccc ggaagcta

48

204070 "ATGAGGCT"

<210> 46
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
primer

<400> 46
gcttcagcag cccatctagc gcaggtcgtc acgttcgctc ttacaacc 48

<210> 47
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
primer

<400> 47
gttcggttggc gcaaactgtt cagctttacc aagtacttcc tgaaaatc 48

<210> 48
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
primer

<400> 48
tcgaaaaaaaa cggtaaagtt tctgggac 28

<210> 49
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
primer

<400> 49
gatgggctgc tgaagctaga gctggagctg ttggtagctt ccggggaa 48

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
primer

304070" aTae00T

<400> 50
aacagtttgc gccaacgaac atcacctgt aagtgggtgt aagag 45

<210> 51
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 51
ttcttgggtcc cagaaacttt accgtttttt tcgattttca ggaagta 47

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 52
ttcttgggtcc cagaaacttt accg 24

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
primer

<400> 53
agatcaggct tctattatta tgagtgtacc accattggaa gaaag 45

<210> 54
<211> 525
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(522)

<400> 54
atg act tgc cag gca ctg ggt caa gac atg gtt tcc ccg gaa gct acc 48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15

aac agc tcc agc tct agc ttc agc agc cca tct agc gca ggt cgt cac 96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30

ggt cgc tct tac aac cac tta cag ggt gat gtt cgt tgg cgc aaa ctg 144

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Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	
		35					40					45				
ttc	agc	ttt	acc	aag	tac	ttc	ctg	aaa	atc	gaa	aaa	aac	ggt	aaa	ggt	192
Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	
	50					55				60						
tct	ggg	acc	aag	aag	gag	aac	tgc	ccg	tac	agc	atc	ctg	gag	ata	aca	240
Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	
	65				70					75					80	
tca	gta	gaa	atc	gga	ggt	ggt	gcc	gtc	aaa	gcc	att	aac	agc	aac	tat	288
Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	
				85					90					95		
tac	tta	gcc	atg	aac	aag	aag	ggg	aaa	ctc	tat	ggc	tca	aaa	gaa	ttt	336
Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	
			100					105					110			
aac	aat	gac	tgt	aag	ctg	aag	gag	agg	ata	gag	gaa	aat	gga	tac	aat	384
Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	
		115					120					125				
acc	tat	gca	tca	ttt	aac	tgg	cag	cat	aat	ggg	agg	caa	atg	tat	gtg	432
Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	
	130					135					140					
gca	ttg	aat	gga	aaa	gga	gct	cca	agg	aga	gga	cag	aaa	aca	cga	agg	480
Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	
	145				150					155					160	
aaa	aac	acc	tct	gct	cac	ttt	ctt	cca	atg	gtg	gta	cac	tca	tag		525
Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser			
				165					170							
<210> 55																
<211> 174																
<212> PRT																
<213> Escherichia coli																
<400> 55																
Met	Thr	Cys	Gln	Ala	Leu	Gly	Gln	Asp	Met	Val	Ser	Pro	Glu	Ala	Thr	
	1			5					10					15		
Asn	Ser	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Ser	Ser	Ala	Gly	Arg	His	
			20					25					30			
Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	
		35					40					45				
Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	
	50					55				60						
Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	
	65				70					75					80	
Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	
				85					90					95		
Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	
			100					105					110			

100363400

Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
 115 120 125
 Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
 130 135 140
 Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
 145 150 155 160
 Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
 165 170

<210> 56
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 56
 ggaccctcat gacctgccag gctctgggtc aggac 35

<210> 57
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 57
 ggacagccat ggctggctgt cacgttcg 28

<210> 58
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 58
 ggacagccat gggttcgttg cgtaaactg 29

<210> 59
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 59
 ggacagccat ggaaaaaac ggtaaagttt c 31

204070" 272300T

<210> 60
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 60
ggacccccat ggagaactgc ccgtagagc 29

<210> 61
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 61
ggacccccat ggtcaaagcc attaacagca ac 32

<210> 62
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 62
ggacccccat ggggaaactc tatggctcaa aag 33

<210> 63
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 63
ctgcccaagc ttattatgag tgtaccacca ttggaag 37

<210> 64
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 64
ctgcccaagc ttattacttc agcttacagt cattgt 36

<210> 65
<211> 525

004070 01040

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(522)

<400> 65
atg acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa gct acc 48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15

aac tct tcc tct tcc tct ttc tct tcc ccg tct tcc gct ggt cgt cac 96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30

gtt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt aaa ctg 144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45

ttc tct ttc acc aaa tac ttc ctg aaa atc gaa aaa aac ggt aaa gtt 192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60

tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca 240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80

tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat 288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95

tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt 336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110

aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga tac aat 384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125

acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg tat gtg 432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140

gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca cga agg 480
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160

aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca tag 525
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

<210> 66
<211> 174
<212> PRT
<213> Homo sapiens

<400> 66
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15

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Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

<210> 67
<211> 444
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(444)

<400> 67
atg gct ggt cgt cac gtt cgt tct tac aac cac ctg cag ggt gac gtt 48
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
1 5 10 15
cgt tgg cgt aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa atc gaa 96
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
20 25 30
aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg tac agc 144
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
35 40 45
atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc 192
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
50 55 60
att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat 240
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
65 70 75 80

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<210> 68
<211> 147
<212> PRT
<213> Homo sapiens
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<400> 68
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
  1                    5                10            15
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
          20                25            30
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
      35                40            45
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
    50                55            60
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
  65                70            75            80
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu
          85                90            95
Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly
      100                105            110
Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly
          115                120            125
Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val
    130                135            140
Val His Ser
  145

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<210> 69
<211> 402
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1)..(402)
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<400> 69
atg gtt cgt tgg cgt aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa 48
Met Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys

1	5	10	15	
atc gaa aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg				96
Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro	20	25	30	
tac agc atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc				144
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val	35	40	45	
aaa gcc att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa				192
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys	50	55	60	
ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag gag agg				240
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg	65	70	75	80
ata gag gaa aat gga tac aat acc tat gca tca ttt aac tgg cag cat				288
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His	85	90	95	
aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga gct cca agg				336
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg	100	105	110	
aga gga cag aaa aca cga agg aaa aac acc tct gct cac ttt ctt cca				384
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro	115	120	125	
atg gtg gta cac tca tag				402
Met Val Val His Ser	130			
<210> 70				
<211> 133				
<212> PRT				
<213> Homo sapiens				
<400> 70				
Met Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys	1	5	10	15
Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro	20	25	30	
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val	35	40	45	
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys	50	55	60	
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg	65	70	75	80
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His	85	90	95	
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg	100	105	110	
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro	115	120	125	
Met Val Val His Ser	130			

204070 "2125001

<210> 71
 <211> 354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(354)

<400> 71
 atg gaa aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg 48
 Met Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro
 1 5 10 15
 tac agc atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc 96
 Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val
 20 25 30
 aaa gcc att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa 144
 Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys
 35 40 45
 ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag gag agg 192
 Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg
 50 55 60
 ata gag gaa aat gga tac aat acc tat gca tca ttt aac tgg cag cat 240
 Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His
 65 70 75 80
 aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga gct cca agg 288
 Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg
 85 90 95
 aga gga cag aaa aca cga agg aaa aac acc tct gct cac ttt ctt cca 336
 Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro
 100 105 110
 atg gtg gta cac tca tag 354
 Met Val Val His Ser
 115

<210> 72
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 72
 Met Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro
 1 5 10 15
 Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val
 20 25 30
 Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys
 35 40 45
 Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg
 50 55 60
 Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His
 65 70 75 80
 Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg
 85 90 95
 Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro

1003542 "010403"

110

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<220>
<221> CDS
<222> (1)..(321)
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<400>	73																
atg	gag	aac	tgc	cgc	tac	agc	atc	ctg	gag	ata	aca	tca	gta	gaa	atc		48
Met	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	Val	Glu	Ile		
1				5					10					15			
gga	gtt	gtt	gcc	gtc	aaa	gcc	att	aac	agc	aac	tat	tac	tta	gcc	atg		96
Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	Leu	Ala	Met		
			20					25					30				
aac	aag	aag	ggg	aaa	ctc	tat	ggc	tca	aaa	gaa	ttt	aac	aat	gac	tgt		144
Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys		
		35					40					45					
aag	ctg	aag	gag	agg	ata	gag	gaa	aat	gga	tac	aat	acc	tat	gca	tca		192
Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	Ser		
	50					55					60						
ttt	aac	tgg	cag	cat	aat	ggg	agg	caa	atg	tat	gtg	gca	ttg	aat	gga		240
Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	Gly		
65					70					75					80		
aaa	gga	gct	cca	agg	aga	gga	cag	aaa	aca	cga	agg	aaa	aac	acc	tct		288
Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr	Ser		
				85					90					95			
gct	cac	ttt	ctt	cca	atg	gtg	gta	cac	tca	tag							321
Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser								
			100					105									

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<210> 74
<211> 106
<212> PRT
<213> Homo sapiens
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<400>	74															
Met	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	Val	Glu	Ile	
1				5					10					15		
Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	Leu	Ala	Met	
			20					25					30			
Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys	
.		35					40					45				
Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	Ser	
	50				55						60					
Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	Gly	
65				70						75					80	
Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr	Ser	

95

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<220>
<221> CDS
<222> (1)..(261)
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<210> 76
<211> 87
<212> PRT
<213> Homo sapiens
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<400> 76
Met Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys
  1                    5                10                15

Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
      20                25                30

Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp
      35                40                45

Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala
      50                55                60

Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe
      65                70                75                80

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Leu Pro Met Val Val His Ser
85

<210> 77
<211> 219
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(219)

<400> 77
atg ggg aaa ctc tat ggc tca aaa gaa ttt aac aat gac tgt aag ctg 48
Met Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
1 5 10 15
aag gag agg ata gag gaa aat gga tac aat acc tat gca tca ttt aac 96
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn
20 25 30
tgg cag cat aat ggg agg caa atg tat gtg gca ttg aat gga aaa gga 144
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly
35 40 45
gct cca agg aga gga cag aaa aca cga agg aaa aac acc tct gct cac 192
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
50 55 60
ttt ctt cca atg gtg gta cac tca tag 219
Phe Leu Pro Met Val Val His Ser
65 70

<210> 78
<211> 72
<212> PRT
<213> Homo sapiens

<400> 78
Met Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
1 5 10 15
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn
20 25 30
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly
35 40 45
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
50 55 60
Phe Leu Pro Met Val Val His Ser
65 70

<210> 79
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (1)..(357)

<400> 79

atg acc tgc cag gct ctg ggt cag gac atg gtt tct ccg gaa gct acc 48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15

aac tct tcc tct tcc tct ttc tct tcc ccg tct tcc gct ggt cgt cac 96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30

gtt cgt tct tac aac cac ctg cag ggt gac gtt cgt tgg cgt aaa ctg 144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45

ttc tct ttc acc aaa tac ttc ctg aaa atc gaa aaa aac ggt aaa gtt 192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60

tct ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag ata aca 240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80

tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc aac tat 288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95

tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa gaa ttt 336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110

aac aat gac tgt aag ctg aag 357
Asn Asn Asp Cys Lys Leu Lys
115

<210> 80

<211> 119

<212> PRT

<213> Homo sapiens

<400> 80

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15

Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45

Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110

100521022500

Asn Asn Asp Cys Lys Leu Lys
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<210> 81
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(276)

<400> 81
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Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
1 5 10 15

cgt tgg cgt aaa ctg ttc tct ttc acc aaa tac ttc ctg aaa atc gaa 96
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
20 25 30

aaa aac ggt aaa gtt tct ggg acc aag aag gag aac tgc ccg tac agc 144
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
35 40 45

atc ctg gag ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc 192
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
50 55 60

att aac agc aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat 240
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
65 70 75 80

ggc tca aaa gaa ttt aac aat gac tgt aag ctg aag 276
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
85 90

<210> 82
<211> 92
<212> PRT
<213> Homo sapiens

<400> 82
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
1 5 10 15

Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
20 25 30

Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
35 40 45

Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
50 55 60

Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
65 70 75 80

Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys

1003512.010403

85

90

<210> 83
<211> 525
<212> DNA
<213> Homo sapiens

<400> 83
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tctcttttct cttccccgtc ttccgctggg cgtcacgttc gttcttataa ccacctgcag 120
ggtgacgttc gttggcgtaa actgttctct ttcaccaaact acttcttgaa aatcgaaaaa 180
aacggtaaaag tttctgggac caagaaggag aactctccgt acagcatcct ggagataaca 240
tcagtagaaa tcggagtgtg tgcggtcaaa gccattaaca gcaactatta cttagccatg 300
aacaagaagg ggaaactcta tggctcaaaa gaatttaaca atgactgtaa gctgaaggag 360
aggatagagg aaaatggata caatacctat gcatcattta actggcagca taatgggagg 420
caaatgtatg tggcattgaa tggaaaagga gctccaagga gaggacagaa aacacgaagg 480
aaaaacacct ctgctcactt tcttccaatg gtggtacact catag 525

<210> 84
<211> 525
<212> DNA
<213> Homo sapiens

<400> 84
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tctcttttct cttccccgtc ttccgctggg cgtcacgttc gttcttataa ccacctgcag 120
ggtgacgttc gttggcgtaa actgttctct ttcaccaaact acttcttgaa aatcgaaaaa 180
aacggtaaaag tttctgggac caagaaggag aactctccgt acagcatcct ggagataaca 240
tcagtagaaa tcggagtgtg tgcggtcaaa gccattaaca gcaactatta cttagccatg 300
aacaagaagg ggaaactcta tggctcaaaa gaatttaaca atgactgtaa gctgaaggag 360
aggatagagg aaaatggata caatacctat gcatcattta actggcagca taatgggagg 420
caaatgtatg tggcattgaa tggaaaagga gctccaagga gaggacagaa aacacgaagg 480
aaaaacacct ctgctcactt tcttccaatg gtggtacact catag 525

<210> 85
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 85
ggaccctcat gacctctcag gctctgggt 29

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 86
aaggagaact ctccgtacag c 21

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<210> 87
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 87
gctgtacggt ctgttctcct t 21

<210> 88
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 88
ggaccctcat gacctgccag gctctgggtc aggac 35

<210> 89
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 89
ctgcccgaagc ttattatgag tgtaccacca ttggaag 37

<210> 90
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 90
aaaggatcct gccaggctct gggtcaggac atg 33

<210> 91
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 91
gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 92
<211> 28

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 92
gggcccgaagc ttatgagtgt accaccat 28

<210> 93
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 93
ccggcggatc ccatatgtct tacaaccacc tgcagg 36

<210> 94
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 94
ccggcggtag cttattatga gtgtaccacc attgg 35

<210> 95
<211> 426
<212> DNA
<213> Homo sapiens

<400> 95
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tactttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atgggtcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcattcattt 300
aactggcagc ataattgggag gcaaatgtat gtggcattga atggaaaagg agctccaagg 360
agaggacaga aaacacgaag gaaaaacacc tctgtctact ttcttccaat ggtggtacac 420
tcataa 426

<210> 96
<211> 141
<212> PRT
<213> Homo sapiens

<400> 96
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

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<400> 99
gggcccaagc ttaagagtgt accaccattg gcagaaagtg agcagaggtg tttttacgac 60
gggtttttctg accacg                                     76
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<210> 100
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 100
gccacataca tttgtcgacc gtt 23

<210> 101
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 101
gggcccaagc ttaagagtg 19

<210> 102
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 102
gccacataca tttgtcgacc gtt 23

<210> 103
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 103
ctgcagggtg acgttcggtg gcgtaaactg ttctccttca ccaaatactt cctgaaaatc 60
gaaaaaaacg gtaaagtttc tggtagcaag 90

<210> 104
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

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<400> 104
agctttaaca gcaacaacac cgatttcaac ggaggtgatt tccaggatgg agtacgggca 60
gttttctttc ttggtaccag aaactttacc 90

<210> 105
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 105
ggtgtgtgtg ctgttaaagc tatcaactcc aactactacc tggctatgaa caagaaaggt 60
aaactgtacg gttccaaaga atttaacaac 90

<210> 106
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 106
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gttctttcag ttacagtcg ttgttaaatt ctttggaacc 100

<210> 107
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 107
gcggcgtcga ccgttgtgct gccag 25

<210> 108
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 108
gcggcctgca gggtgacgtt cgttgg 26

<210> 109
<211> 36
<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 109

ccggcgggatc ccatatgtct tacaaccacc tgcagg 36

<210> 110

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 110

cgcgcgatat cttattaaga gtgtaccacc attg 34

<210> 111

<211> 426

<212> DNA

<213> Homo sapiens

<400> 111

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tacttcctga aaatcgaaaa aaacggtaaa gtttctggta ccaagaaaga aaactgcccg 120
tactccatcc tggaaatcac ctccgttgaa atcgggtgtg ttgctgttaa agctatcaac 180
tccaactact acctggctat gaacaagaaa ggtaaaactgt acgggttccaa agaatttaac 240
aacgactgta aactgaaaga acgtatcgaa gaaaacgggtt acaacaccta cgcttccttc 300
aactggcagc acaacggtcg acaaatgtat gtggcactga acggtaaagg tgctccacgt 360
cgtggtcaga aaaccgctcg taaaaacacc tctgctcact ttctgccaat ggtggtacac 420
tcttaa 426

<210> 112

<211> 141

<212> PRT

<213> Homo sapiens

<400> 112

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

004010"2F35001

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 113
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 113
cgcgcccatg gctctggggtc aggacatg 28

<210> 114
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 114
gggcccaagc ttatgagtgt accaccat 28

<210> 115
<211> 516
<212> DNA
<213> Homo sapiens

<400> 115
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tcttccccgt cttccgctgg tcgtcacggt cgttcttaca accacctgca gggtgacgtt 120
cgttggcgta aactgttctc tttcaccaaa tacttctctga aaatcgaaaa aaacggtaaa 180
gtttctggga ccaagaagga gaactgcccg tacagcatcc tggagataac atcagtagaa 240
atcggagttg ttgcccgtcaa agccattaac agcaactatt acttagccat gaacaagaag 300
gggaaactct atggctcaaa agaatttaac aatgactgta agctgaagga gaggatagag 360
gaaaatggat acaataccta tgcattcattt aactggcagc ataatgggag gcaaatgtat 420
gtggcattga atggaaaagg agctccaagg agaggacaga aaacacgaag gaaaaacacc 480
tctgtcact ttcttccaat ggtggtacac tcataa 516

<210> 116
<211> 171
<212> PRT
<213> Homo sapiens

<400> 116
Met Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser
1 5 10 15

204010"2125001

Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser
20 25 30
Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe
35 40 45
Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr
50 55 60
Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu
65 70 75 80
Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala
85 90 95
Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp
100 105 110
Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala
115 120 125
Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn
130 135 140
Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr
145 150 155 160
Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

<210> 117

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 117

gcgggcacatg tcttacaacc acctgcaggg tg

32

<210> 118

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 118

ctgcccaagc ttttatgagt gtaccacat tggaagaaag tgagcagagg tgtttttttc 60
tcgtgttttc tgtcc 75

<210> 119

<211> 426

<212> DNA

<213> Homo sapiens

<400> 119

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atgtcttaca accacctgca ggggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
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tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atgggtcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcattcatt 300
aactggcagc ataatgggag gcaaattgtat gtggcattga atggaaaagg agctccaagg 360
agaggacaga aaacacgaga aaaaaacacc tctgtctact ttcttccaat ggtggtacac 420
tcatag

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<210> 120
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 120
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 1 5 10 15
 Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
 20 25 30
 Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
 35 40 45
 Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
 50 55 60
 Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
 65 70 75 80
 Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
 85 90 95
 Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
 100 105 110
 Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Glu Lys
 115 120 125
 Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
 130 135 140

<210> 121
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 121
 gcggcacatg tcttacaacc acctgcaggg tg 32

<210> 122
 <211> 75
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Description of Artificial Sequence: primer

<400> 122
ctgccaagc ttttatgagt gtaccacat tggaagaaag tgagcagagg tgtttttctg 60
tcgtgttttc tgtcc 75

<210> 123
<211> 426
<212> DNA
<213> Homo sapiens

<400> 123
atgtcttaca accacctgca ggggtgacgtt cgttggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgccc 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcattcatt 300
aactggcagc ataatgggag gcaaatgtat gtggcattga atggaaaagg agctccaagg 360
agaggacaga aaacacgaca gaaaaacacc tctgtcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 124
<211> 141
<212> PRT
<213> Homo sapiens

<400> 124
Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Gln Lys
115 120 125
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 125
<211> 32
<212> DNA
<213> Artificial Sequence

204010"2125E001

<220>

<223> Description of Artificial Sequence: primer

<400> 125

gcggcacatg tcttacaacc acctgcaggg tg

32

<210> 126

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 126

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tcgtgtttcc tgcctctccc ttgg 84

<210> 127

<211> 426

<212> DNA

<213> Homo sapiens

<400> 127

atgtctttaca accacctgca ggggtgacgtt cggtggcgta aactgtttctc tttcaccaaaa 60
tactttcctga aaatcgaaaa aaacgggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaaa agaatttaac 240
aatgactgta agctgaagga gaggatagag gaaaatggat acaataccta tgcattcattt 300
aactggcagc ataatgggag gcaaattgtat gtggcattga atggaaaagg agctccaagg 360
agaggacagg aaacacgaag gaaaaacacc tctgctcact ttcttccaat ggtggtacac 420
tcatag 426

<210> 128

<211> 141

<212> PRT

<213> Homo sapiens

<400> 128

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15

Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

204070 273300

Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45

Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60

Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Gln Thr Arg Arg Lys
115 120 125

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

<210> 133
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 133
gcggcacatg tottacaacc acctgcaggg tg 32

<210> 134
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 134
ctgcccgaagc ttttatgagt gtaccacat tggaagaaag tgagcagagg tgtttttct 60
tcgtgttttc tgccttccc ttgagctcc ttt 93

<210> 135
<211> 426
<212> DNA
<213> Homo sapiens

<400> 135
atgtcttaca accacctgca gggtagcgtt cggtggcgta aactgttctc tttcaccaaa 60
tacttcctga aaatcgaaaa aaacggtaaa gtttctggga ccaagaagga gaactgcccg 120
tacagcatcc tggagataac atcagtagaa atcggagttg ttgccgtcaa agccattaac 180
agcaactatt acttagccat gaacaagaag gggaaactct atggctcaa agaatttaac 240
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tcatag 426

<210> 136
<211> 140

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<210> 140
<211> 141
<212> PRT
<213> Homo sapiens
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<210> 141
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<212> DNA
<213> Artificial Sequence
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<400> 141
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<210> 142
<211> 21
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<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: primer

<400> 142
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<210> 143
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 143
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<210> 144
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 144
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<210> 145
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<212> DNA
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aactggcagc ataatgggag gcaaatgtat gtggcattga atggagaagg agctccaagg 360
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tcatag 426

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<211> 141
<212> PRT
<213> Homo sapiens

<400> 146
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Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
      35          40          45

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Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
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Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80

Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95

Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110

Leu Asn Gly Glu Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
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Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
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<210> 147

<211> 3974

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pHE4-5 vector

<400> 147

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gccatgtccg	gttttcaaca	aaccatgcaa	atgctgaatg	agggcatcgt	tcccactcgg	1980
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<210> 148
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: pHE4-5
 promoter sequence

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<400> 148
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<210> 149
 <211> 106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

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<400> 149
gagcgcggat ccgccacat gaaggtctcc gtggctgcc tctcctgcct catgcttggt 60
actgcccttg gatctcaggc cagctacaat caccttcaag gagatg 106

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20250312 10:56:07

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$\langle 211 \rangle$	32

<213> Artificial Sequence

<223> Description of Artificial Sequence: primer

32

<213> Artificial Sequence

<223> Description of Artificial Sequence: primer

39

<213> Artificial Sequence

<223> Description of Artificial Sequence: primer

32

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<223> Description of Artificial Sequence: primer

39

<213> Artificial Sequence

<223> Description of Artificial Sequence: primer

32

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160
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<210> 161
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161
gatcgcggtat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 162
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 162
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<210> 163
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 163
gatcgcggtat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 164
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 164
gatcgctcta gattatgagt gtaccacat tggaagaaag 40

<210> 165
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 165
gatcgcggtat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 166
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 166
gatcgctcta gattatgagt gtaccaccat tggaagaaag 40

<210> 167
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 167
gatcgcggtat ccgccaccat gtggaaatgg atactgacac attgtgc 47

<210> 168
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 168
gatcgctcta gattatgagt gtaccaccat tggaagaaag 40

<210> 169
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 169
gatcgccata tggctggtcg tcacgttcgt tc 32

<210> 170
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 170
gatcgcggtat ccttattatg agtgtaccac cattggaag 39

<210> 171
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 171
gatcgccata tggctggtcg tcaogttcgt tc 32

<210> 172
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 172
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<210> 173
<211> 456
<212> DNA
<213> Escherichia coli

<400> 173
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accaagaagg agaactgcc gtacagcatc ctggagataa catcagtaga aatcggagtt 180
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tacaatacct atgcatcatt taactggcag cataatggga ggcaaatgta tgtggcattg 360
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<210> 174
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 174
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<210> 175
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 175

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47

<210> 176

<211> 447

<212> DNA

<213> Escherichia coli

<400> 176

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ctgccgatgg	ttgtacactc	ataataa				447

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